

1 ATGAGCTTCCTAGAGCAAGGAGAGAGCCGTTTCATGGCCATCCCGAGCTGTAACCACCAGCTCAGAAAGAA
M S F L E Q G E S R S W P S R A V T T S S E R
30
Acc
T
71 GCCATGGGGACCAGGGGAaCAAGGCCTCTAGATGGACAAGGCAGGAGGATGTAGAGGAAGGGGGGCTCC
S H G D Q G N K A S R W T R Q E D V E E G G P P
52
aGT
S
141 GGGCCCGAGGGAAGTCCCCAGTCCAGGCCAGTTGCTGAGTCCACCGGGCAGGAGGCCACATTCCCCAAG
G P R E G P Q S R P V A E S T G Q E A T F P K
211 GCCACACCCCTTGGCCCAAGCCGCTCCCTTGGCCGAGGTGGACAACCCCCCAACAGAGCGGGACATCCTCC
A T P L A Q A A P L A E V D N P P T E R D I L
281 CCTCTGACTGTGCAGCCTCAGCCTCCGACTCCAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGC
P S D C A A S A S D S N T D H L D L G I E F S A
351 CTCGGCGGCGTCGGGGATGAGCTTGGGCTGGTGGGAAGAGAAGCCAGCCCCGTGCCCATCCCCAGAGGTG
S A A S G D E L G L V E E K P A P C P S P E V
421 CTGTTACCCAGGCTGGGCTGGGATGATGAGCTGCAGAAGCCGGGGGCCAGGTCTACATGCACTTCATGC
L L P R L G W D D E L Q K P G A Q V Y M H F M
491 AGGAGCACACCTGTCTACGATGCCATGGCGACCAGCTCCAAACTGGTTCATCTTCGACACCATGCTGGAGAT
Q E H T C Y D A M A T S S K L V I F D T M L E I
199200
aTCCaA
I Q
561 CAAGAAGGCCTTCTTTGCCCTGGTGGCCAACGGCGTCCgAGCGGCACCTTTGTGGGACAGCAAGAAGCAG
K K A F F A L V A N G V R A A P L W D S K K Q
631 AGCTTCGTGGGGATGCTGACCATCACAGACTTCATCTTGGTGTCTGCACCGCTATTACAGGTCCCCCTGG
S F V G M L T I T D F I L V L H R Y Y R S P L
701 TCCAGATCTACGAGATTGAAGAACATAAGATTGAGACCTGGAGGGAGATCTACCTTCAAGCTGTCTTCAA
V Q I Y E I E E H K I E T W R E I Y L Q G C F K
771 GCCTCTGGTCTCCATCTCTCCAATGACAGCCTGTTGGAAGCTGTCTACGCCCTCATCAAGAACCGGATC
P L V S I S P N D S L F E A V Y A L I K N R I
841 CACCGCCTGCCGGTCTCTGGACCCTGTCTCCGGGGCTGTGCTCCACATCCTCACACATAAGCGGCTTCTCA
H R L P V L D P V S G A V L H I L T H K R L L
911 AGTTCCTGCACATCTTTGGCACCCCTGTGCCCCGGCCCTCCTTCTCTACCGCACCATCCAAGATTGTTGGG
K F L H I F G T L L P R P S F L Y R T I Q D L G
981 CATCGGCACATTCGAGACTTGGCCGTGGTGTCTGGAACGGCGCCCATCTGACCGCACTGGACATCTTC
I G T F R D L A V V L E T A P I L T A L D I F
051 GTGGACCGGCGTGTGTCTGCGCTGCCCTGTGGTCAACGAAACTGGACAGGTAGTGGGCCTCTACTCTCGCT
V D R R V S A L P V V N E T G Q V V G L Y S R
1121 TTGATGTGATCCACCTGGCTGCCCAACAAACATAACAACCCTGGACATGAATGTGGGAGAAGCCCTGAG
F D V I H L A A Q Q T Y N H L D M N V G E A L R
1191 GCAGCGGACACTGTGTCTGGAAGGCGTCCTTTCTGCCAGCCCCACGAGACCTTGGGGGAAGTCATTGAC
Q R T L C L E G V L S C Q P H E T L G E V I D
1261 CGGATTGTCCGGAACAGGTGCACCGCCTGGTGTCTGGATGAGACCCAGCACCTTCTGGGCGTGGTGT
R I V R E Q V H R L V L V D E T Q H L L G V V
1331 CCCTCTCTGACATCCTTCAGGCTCTGGTGTCTGAGCCCTGCTGGAATTGATGCCCTCGGGGCTGAGAACC
S L S D I L Q A L V L S P A G I D A L G A *
1401 TTGGAACCTTTGCTCTCAGGCCACCTGGCACACCTGGAAGCCAGTGAAGGGAGCCGTGGACTCAGCTCTC
1471 ACTTCCCCTCAGCCCCACTTGCTGGTCTGGCTCTTGTTCAGGTAGGCTCCGCCCCGGGGCCCTGGCCTCA
1541 GCATCAGCCCCCTCAGTCTCCCTGGGCACCCAGATCTCAGACTGGGGCACCTGAAGATGGGAGTGGCCCA
1611 GCTTATAGCTGAGCAGCCTTGTGAAATCTACCAGCATCAAGACTCACTGTGGGACCACTGCTTTGTCCCA
1681 TTCTCAGCTGAAATGATGGAGGGCCTCATAAGAGGGGTGGACAGGGCCTGGAGTAGAGGCCAGATCAGTG
1751 ACGTGCCTTCAGGACCTCCGGGGAGTTAGAGCTGCCCTCTCTCAGTTCACTTCCCCCTGCTGAGAATGT
1821 CCCTGGAAGGAAGCCAGTTAATAAACCTTGGTTGGATGGAATTGGAGAGTCCG

Fig. 1

GAAACTCTTCTCCCCACAG**ACTCCCTCCTGGAGCAGCCTCGGGGGACCTAAGC**
ATCAAGGTAGGTGGGGCTGCCCCTGCTCGCGGGCCCAGGCTCTTCTCCACCT
CCTTTTCTTCCACGTCTTCAGGACCCCAATCTCCCCACTCCACTCGCCTGGCT
CTTGTCTTCCTCTCCTTTGCCTTCTTTGTTCCGCTTTGTTTCTTCTTCCTCCCTCT
CCCTCACCTCCTCCCTCTTTCAAAAGAGTAGAGGGGGCATCTATAGAGTCTGG
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AAATTGCTTCACCTCTCTGAGCTCAGGTCTCTCGTTAGTAAACAGGGCT
GATAGCCATGCCCTTCGGATAAGATTGCCGTGAGGGTTGAATGAGAAATT
TGTTGGAGGACAAGCCCTTTGAAGCT**TCCCAATATTAAATATTTTTATTT**
ATTTATTTATTTTTTTGTCTTTTTGCTATTCCCTTTGGGCCGCTCCACGGC
ATATGGAGGTTCCCAGGCTAGGGGTCGAATCGGAGCTGTAGCCACTGGCC
TACGCCAGAGCCACAGCAACGCGGGATCCGAGCCGCATCTGCAACCTACA
CCACAGCTCACGGCAACGCCGGATCGTTAACCCTGAGCAGGGGCAGGC
ACCGAACCTGCAACCTCATGGTTCCTAGTGGGATTCGTTAACCCTGCGC
CACGACGGGA**ACTCCCAATATTAAATATTATTATTAGTAACATTTAAT**
GGAATTTATTGTGTTACTCCCCATTAACCAAACAGGTCCCATTCTCCCTT
GCAGAGAT**GAGCTTCCTAGAGCAAGGAGAGAGCCGTT**CATGGCCAT**CCCCG**
AGCTGTGACCACCAGCTCAGAAAGAAGCCATGGGGACCAGGGGACCAAGG
CCTCTAGATGGACAAGGCAGGAGGATRAGAGGAAGGGGGGCCTCCGGGC
CCGAGGGAARGTGAGTTCAAGGCCAGTTCTGGGGAGCTGGGACTGGGGGC
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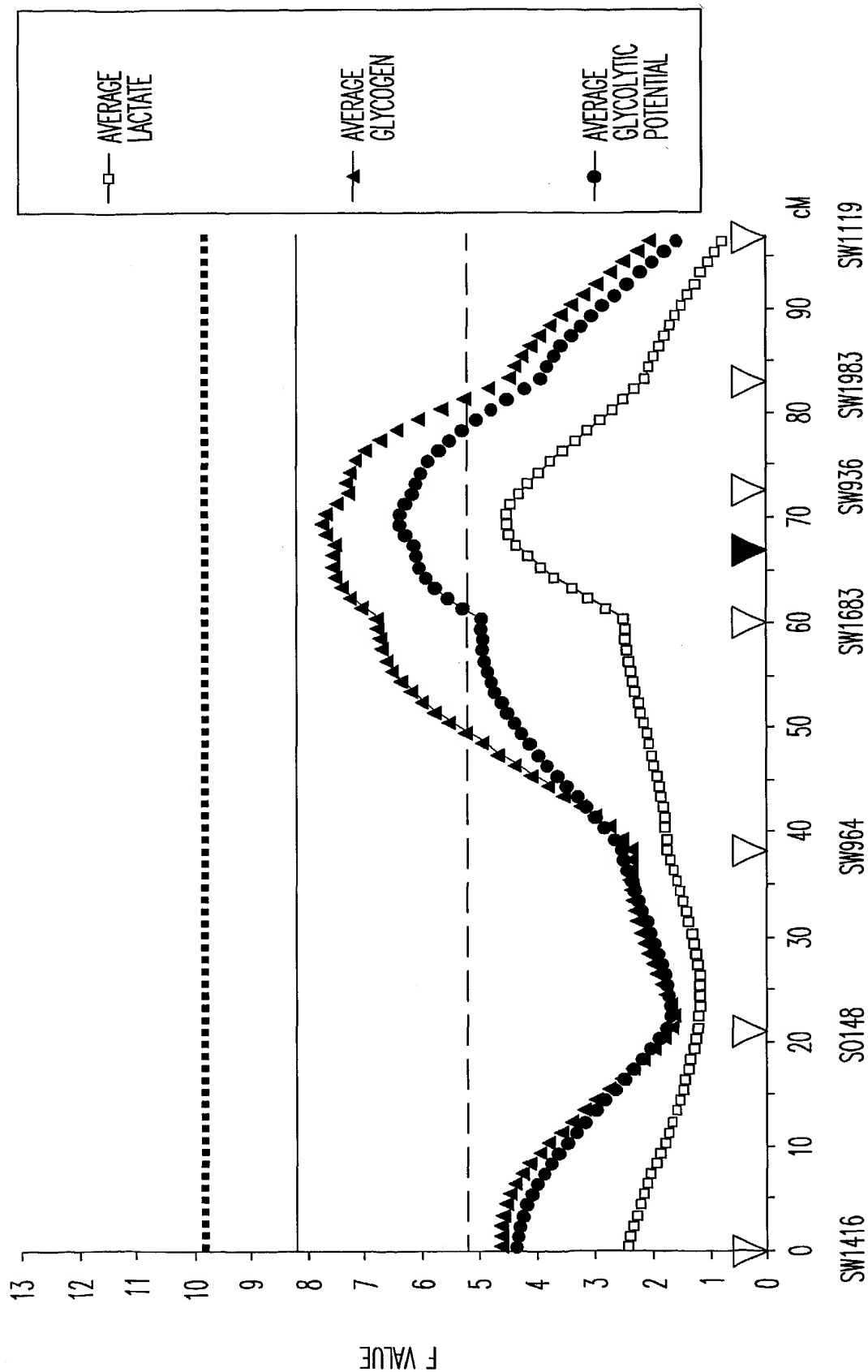
Fig. 2A

090002-0001

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TAGCTGTGTGATTTGTGGCAAATTGCTTCACCTCTCTGAGCTCAGGTCTC
TCGTTAGTAAAACAGGGCTGATAGCCATGCCCTTCGGATAAGATTGCCGT
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GAGCAAGGAGAGAGCCGTTTCATGGCCATCCCGAGCTGTGACCACCAGCTC
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AGGAGGATATAGAGGAAGGGGGGCTCCGGGGCCCGAGGGAARGTGAGTTC
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Fig. 2B

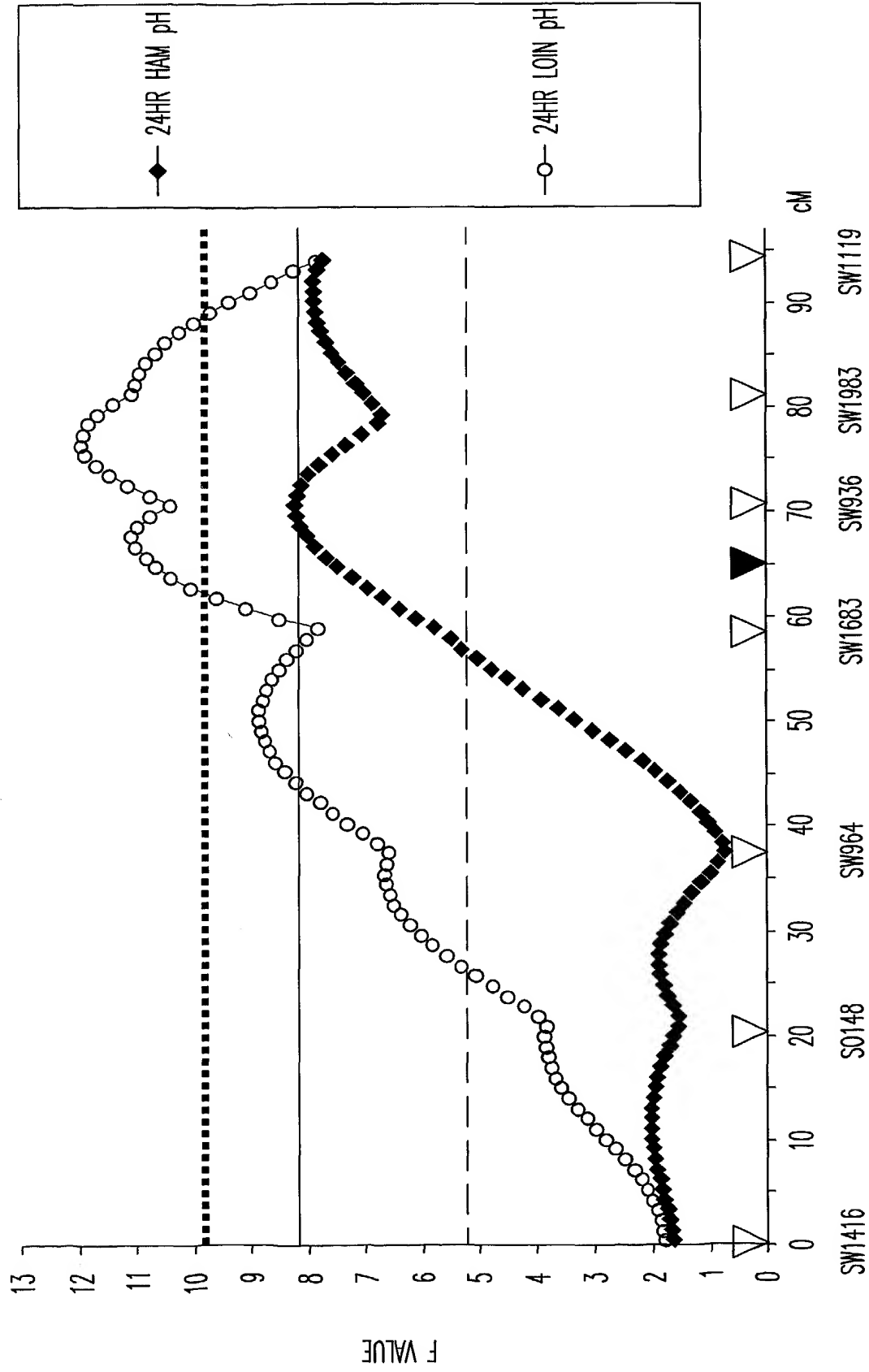
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PRKAG3

Fig. 3A

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PRKAG3

Fig. 3B

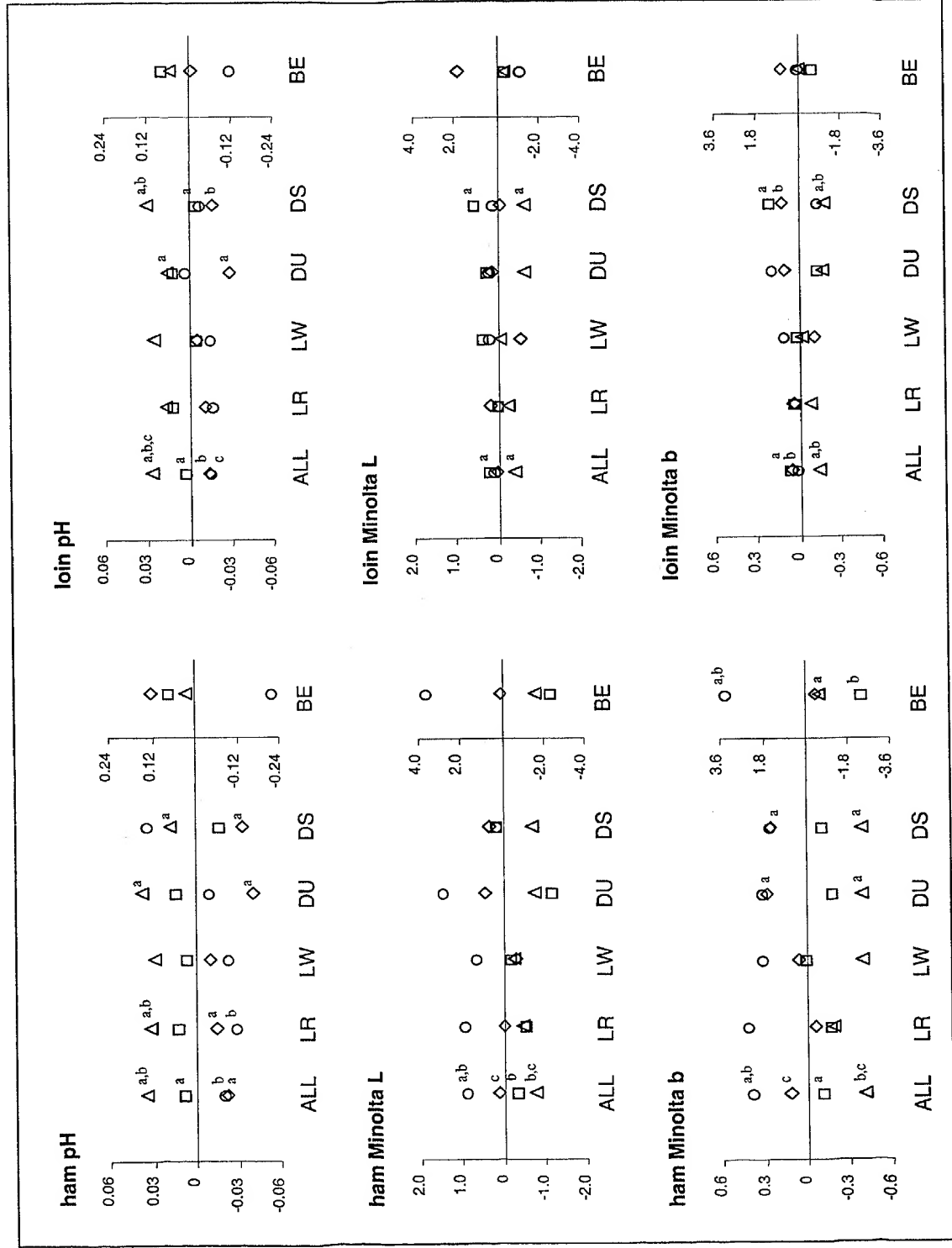


Fig. 4